

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/590,146
Source: IFWP
Date Processed by STIC: 08/30/2006

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IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/590,146

DATE: 08/30/2006

TIME: 09:07:50

Input Set : A:\2006-1392A - Sequence Listing.txt
 Output Set: N:\CRF4\08302006\J590146.raw

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3 <110> APPLICANT: Yamamoto, Hiroshi
4           Konishi, Noboru
6 <120> TITLE OF INVENTION: A method for decision of prostate tumor
8 <130> FILE REFERENCE: 09680
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/590,146
C--> 10 <141> CURRENT FILING DATE: 2006-08-21
10 <150> PRIOR APPLICATION NUMBER: JP 2004-47036
11 <151> PRIOR FILING DATE: 2004-02-23
13 <160> NUMBER OF SEQ ID NOS: 5
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1520
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (407)..(1267)
27 <400> SEQUENCE: 1
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30 tgcacggcg cgcccgctc cgcggcaag tgcgccttcc tgacttactg ctgggtgcgc      120
32 ggggtgggg gtgcgagttac caccctgaa gtctttccct gggcgacctc cggggcctca      180
34 ttcttaggcct ccttaaaagag aaggatctaa attagaaaaa ggaagtgcctt ttatccacga      240
36 ccaagctctt ccacctgcgg agctcgctt gtctgcacct caaccgtgcg gaaagtgact      300
38 gccctgttta ctgagggaaa actggggctc agaaagatac catggagtag tttgaaacag      360
40 gaacaaaatc ttctgaaagc tcggagcaga agccttttg gtcaac atg gag gaa      415
41                               Met Glu Glu
42                               1
44 aaa aga cgg cga gcc cga gtt cag gga gcc tgg gct gcc cct gtt aaa      463
45 Lys Arg Arg Arg Ala Arg Val Gln Gly Ala Trp Ala Ala Pro Val Lys
46      5          10          15
48 agc cag gcc att gct cag cca gct acc act gct aag agc cat ctc cac      511
49 Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser His Leu His
50 20          25          30          35
52 cag aag cct ggc cag acc tgg aag aac aaa gag cat cat ctc tct gac      559
53 Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His Leu Ser Asp
54          40          45          50
56 aga gag ttt gtg ttc aaa gaa cct cag cag gta gta cgt aga gct cct      607
57 Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg Arg Ala Pro
58          55          60          65
60 gag cca cga gtg att gac aga gag ggt gtg tat gaa atc agc ctg tca      655
61 Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile Ser Leu Ser
62          70          75          80
64 ccc aca ggt gta tct agg gtc tgt ttg tat cct ggc ttt gtt gac gtg      703

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65	Pro	Thr	Gly	Val	Ser	Arg	Val	Cys	Leu	Tyr	Pro	Gly	Phe	Val	Asp	Val	
66	85			90						95							
68	aaa	gaa	gct	gac	tgg	ata	ttg	gaa	cag	ctt	tgt	caa	gat	gtt	ccc	tgg	751
69	Lys	Glu	Ala	Asp	Trp	Ile	Leu	Glu	Gln	Leu	Cys	Gln	Asp	Val	Pro	Trp	
70	100			105						110						115	
72	aaa	cag	agg	acc	ggc	atc	aga	gag	gat	ata	act	tat	cag	caa	cca	aga	799
73	Lys	Gln	Arg	Thr	Gly	Ile	Arg	Glu	Asp	Ile	Thr	Tyr	Gln	Gln	Pro	Arg	
74		120					125						130				
76	ctt	aca	gca	tgg	tat	gga	gaa	ctt	cct	tac	act	tat	tca	aga	atc	act	847
77	Leu	Thr	Ala	Trp	Tyr	Gly	Glu	Leu	Pro	Tyr	Thr	Tyr	Ser	Arg	Ile	Thr	
78		135					140					145					
80	atg	gaa	cca	aat	cct	cac	tgg	cac	cct	gtg	ctg	cgc	aca	cta	aag	aac	895
81	Met	Glu	Pro	Asn	Pro	His	Trp	His	Pro	Val	Leu	Arg	Thr	Leu	Lys	Asn	
82		150					155				160						
84	cgc	att	gaa	gag	aac	act	ggc	cac	acc	ttc	aac	tcc	tta	ctc	tgc	aat	943
85	Arg	Ile	Glu	Glu	Asn	Thr	Gly	His	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Asn	
86		165					170				175						
88	ctt	tat	cgc	aat	gag	aag	gac	agc	gtg	gac	tgg	cac	agt	gat	gat	gaa	991
89	Leu	Tyr	Arg	Asn	Glu	Lys	Asp	Ser	Val	Asp	Trp	His	Ser	Asp	Asp	Glu	
90	180		185				190				195						
92	ccc	tca	cta	ggg	agg	tgc	ccc	att	att	gct	tca	cta	agt	ttt	ggt	gcc	1039
93	Pro	Ser	Leu	Gly	Arg	Cys	Pro	Ile	Ile	Ala	Ser	Leu	Ser	Phe	Gly	Ala	
94		200					205				210						
96	aca	cgc	aca	ttt	gag	atg	aga	aag	aag	cca	cca	cca	gaa	gag	aat	gga	1087
97	Thr	Arg	Thr	Phe	Glu	Met	Arg	Lys	Lys	Pro	Pro	Pro	Glu	Glu	Asn	Gly	
98		215					220				225						
100	gac	tac	aca	tat	gtg	gaa	aga	gtg	aag	ata	ccc	ttg	gat	cat	ggg	acc	1135
101	Asp	Tyr	Thr	Tyr	Val	Glu	Arg	Val	Lys	Ile	Pro	Leu	Asp	His	Gly	Thr	
102		230					235				240						
104	ttg	tta	atc	atg	gaa	gga	gcg	aca	caa	gct	gac	tgg	cag	cat	cga	gtg	1183
105	Leu	Leu	Ile	Met	Glu	Gly	Ala	Thr	Gln	Ala	Asp	Trp	Gln	His	Arg	Val	
106		245					250				255						
108	ccc	aaa	gaa	tac	cac	tct	aga	gaa	ccg	aga	gtg	aac	ctg	acc	ttt	cgg	1231
109	Pro	Lys	Glu	Tyr	His	Ser	Arg	Glu	Pro	Arg	Val	Asn	Leu	Thr	Phe	Arg	
110	260		265				270				275						
112	aca	gtc	tat	cca	gac	cct	cga	ggg	gca	ccc	tgg	tga	cgtcagagct			1277	
113	Thr	Val	Tyr	Pro	Asp	Pro	Arg	Gly	Ala	Pro	Trp						
114		280					285										
116	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1337
118	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1397
120	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1457
122	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1517
124	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1520
127	<210>	SEQ	ID	NO:	2												
128	<211>	LENGTH:	286														
129	<212>	TYPE:	PRT														
130	<213>	ORGANISM:	Homo sapiens														
132	<400>	SEQUENCE:	2														
134	Met	Glu	Glu	Lys	Arg	Arg	Ala	Arg	Val	Gln	Gly	Ala	Trp	Ala	Ala		

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135 1           5           10           15
138 Pro Val Lys Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser
139          20          25          30
142 His Leu His Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His
143          35          40          45
146 Leu Ser Asp Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg
147          50          55          60
150 Arg Ala Pro Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile
151 65          70          75          80
154 Ser Leu Ser Pro Thr Gly Val Ser Arg Val Cys Leu Tyr Pro Gly Phe
155          85          90          95
158 Val Asp Val Lys Glu Ala Asp Trp Ile Leu Glu Gln Leu Cys Gln Asp
159          100         105         110
162 Val Pro Trp Lys Gln Arg Thr Gly Ile Arg Glu Asp Ile Thr Tyr Gln
163          115         120         125
166 Gln Pro Arg Leu Thr Ala Trp Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser
167          130         135         140
170 Arg Ile Thr Met Glu Pro Asn Pro His Trp His Pro Val Leu Arg Thr
171 145          150          155          160
174 Leu Lys Asn Arg Ile Glu Glu Asn Thr Gly His Thr Phe Asn Ser Leu
175          165          170          175
178 Leu Cys Asn Leu Tyr Arg Asn Glu Lys Asp Ser Val Asp Trp His Ser
179          180          185          190
182 Asp Asp Glu Pro Ser Leu Gly Arg Cys Pro Ile Ile Ala Ser Leu Ser
183          195          200          205
186 Phe Gly Ala Thr Arg Thr Phe Glu Met Arg Lys Lys Pro Pro Pro Glu
187          210          215          220
190 Glu Asn Gly Asp Tyr Thr Tyr Val Glu Arg Val Lys Ile Pro Leu Asp
191 225          230          235          240
194 His Gly Thr Leu Leu Ile Met Glu Gly Ala Thr Gln Ala Asp Trp Gln
195          245          250          255
198 His Arg Val Pro Lys Glu Tyr His Ser Arg Glu Pro Arg Val Asn Leu
199          260          265          270
202 Thr Phe Arg Thr Val Tyr Pro Asp Pro Arg Gly Ala Pro Trp
203          275          280          285
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 861
208 <212> TYPE: DNA
209 <213> ORGANISM: Homo sapiens
211 <400> SEQUENCE: 3
212 atggagggaaa aaagacggcg agccccgaggc cagggagcct ggggtgcggcc tttttttttt 60
214 caggccattt ctcagccatc taccactgtc aagagccatc tccaccagaa gcctggccag 120
216 accttggaaaga acaaagagca tcatctctt gacagagagt ttgtgttcaa agaacctcag 180
218 caggttagtac gttagagctcc tgagccacga gtgattgaca gagagggtgt gtatgaaatc 240
220 agcctgtcac ccacaggtgt atcttagggtc tttttgtatc ctggctttgt tgacgtgaaa 300
222 gaagctgact ggatatttggaa acagctttgt caagatgttc cctggaaaca gaggaccggc 360
224 atcagagagg atataactta tcagcaacca agacttacag catggtatgg agaacttcct 420
226 tacacttattt caagaatcac tatggAACCA aatcctcaactt ggcaccctgt gctgcgcaca 480
228 ctaaagaacc gcattgaaga gaacactggc cacacccatca actccttactt ctgcaatctt 540

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230 tatcgcaatg agaaggacag cgtggactgg cacagtgatg atgaaccctc actagggagg 600
232 tgccccatta ttgcttcact aagttttgtt gccacacgca catttgagat gagaagaag 660
234 ccaccaccag aagagaatgg agactacaca tatgtggaaa gagtgaagat accttggat 720
236 catgggacct tgttaatcat ggaaggagcg acacaagctg actggcagca tcgagtgcc 780
238 aaagaatacc actctagaga accgagagtg aacctgacct ttcggacagt ctatccagac 840
240 cctcgagggg caccctggta a 861
243 <210> SEQ ID NO: 4
244 <211> LENGTH: 21
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Oligonucleotide designed to act as PCR primer for detection

of

250 PCA-1 gene
252 <400> SEQUENCE: 4
253 ctgaaagctc ggagcagaag c 21
256 <210> SEQ ID NO: 5
257 <211> LENGTH: 18
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Oligonucleotide designed to act as PCR primer for detection

of
263 PCA-1 gene
265 <400> SEQUENCE: 5
266 ggtctactgt gggAACAG 18

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/30/2006
PATENT APPLICATION: US/10/590,146 TIME: 09:07:51

Input Set : A:\2006-1392A - Sequence Listing.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5

VERIFICATION SUMMARY DATE: 08/30/2006
PATENT APPLICATION: US/10/590,146 TIME: 09:07:51

Input Set : A:\2006-1392A - Sequence Listing.txt
Output Set: N:\CRF4\08302006\J590146.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date